



SEQUENCE LISTING

<110> Kato, Seiji
Kimura, Tomoko
O-kine, Shingo
Kobayashi, Midori

<121> HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND GENES
ENCODING THESE PROTEINS

<130> GIN-67112700

<150> JP 9/276,271

<151> 1997-10-01

<140> G9/529,205

<141> 2000-08-21

<160> 48

<170> PatentIn Ver. 2.0

<210> 1

<211> 123

<212> PRT

<213> Homo sapiens

<400> 1

Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
1 5 10 15

Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn
20 25 30

Gln Asp Cys Leu Gln Val Lys Asn Cys Thr Gln Leu Gly Gln Gln Cys
35 40 45

Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
50 55 60

Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly
65 70 75

Iys Iys Asn Ile Thr Tyr Tyr Asp Thr Asp Leu Tyr Asn Ala Ser Gly
80 85 90

Ala His Ala Leu His Pro Ala Ala Ala Ile Leu Ala Leu Ile Pro Ala
95 100 105 110

Leu Gly Leu Leu Leu Trp Gly Pro Gly His Leu
115 120

44088

Met Ser Met Gly Leu Gln Ile Thr Gly Thr Ala Leu Ala Val Leu Gly
1 5 10 15

Trp Leu Gly Thr Ile Val Cys Cys Ala Leu Pro Met Trp Arg Val Ser
20 25 30 35

Ala Phe Ile Gly Ser Asn Ile Ile Thr Ser Gln Asn Ile Trp Glu Gly
40 45 50 55

Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys Lys
60 65 70

Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg
75 80 85

Ala Leu Ile Val Val Ala Ile Leu Leu Ala Ala Phe Gly Leu Leu Val
90 95 100

Ala Leu Val Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala
105 110 115

Lys Ala Lys Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala
120 125 130

Leu Leu Thr Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg
135 140 145

Asp Phe Tyr Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly
150 155 160

Ala Gly Leu Tyr Val Gly Trp Ala Ala Ala Ala Leu Gln Leu Leu Gly
165 170 175

Gly Ala Leu Leu Cys Cys Ser Cys Pro Pro Arg Gln Lys Lys Tyr Thr
180 185 190

Ala Thr Lys Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Phe Gly Ala
195 200 205

Asp Ile Tyr Thr Gly Ser Arg Arg Lys Arg Lys Val
210 215 220

44089

44090

44091

44092 Hemo-sepiens

44093

Met Ala Tyr Gly Gly Ile Thr Val Pro Leu Ile Val Met Ser Val Pro

Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys Cys
 35 40 45

Tyr Leu Ile Thr Leu Ile Ala Ile Leu Ala Gln Leu Asn Pro Leu Thr
 50 55 60

Gly Pro Gln Leu Lys Asn Glu Thr Ile Thr Tyr Leu Lys Tyr His Trp
 65 70 75 80

Pro

<10> 4

<11> 391

<12> 187

<13> Homo sapiens

<100> 4

Met Leu Ala Leu Arg Val Ala Arg Gly Ser Trp Gly Ala Leu Arg Gly
 1 5 10 15

Ala Ala Trp Ala Pro Gly Thr Arg Pro Ser Lys Arg Arg Ala Cys Trp
 20 25 30

Ala Leu Leu Pro Pro Val Pro Cys Cys Leu Gly Cys Leu Ala Glu Arg
 35 40 45

Trp Arg Leu Arg Pro Ala Ala Leu Gly Leu Arg Leu Pro Gly Ile Gly
 50 55 60

Gln Arg Asn His Cys Ser Gly Ala Gly Lys Ala Ala Pro Arg Pro Ala
 65 70 75 80

Ala Gly Ala Gly Ala Ala Ala Glu Ala Pro Gly Gly Gln Trp Gly Pro
 85 90 95

Ala Ser Thr Pro Ser Leu Tyr Glu Asn Pro Trp Thr Ile Pro Asn Met
 100 105 110

Leu Ser Met Thr Arg Ile Gly Leu Ala Pro Val Leu Gly Tyr Leu Ile
 115 120 125

Leu Arg Leu Arg Ile Asn Ile Ala Leu Gly Val Ile Ala Leu Ala Gly
 130 135 140

Leu Thr Arg Leu Leu Arg Gly Ile Ile Ala Arg Asn Trp Asn Asn Thr
 145 150 155

Arg Ser Ala Leu Gly Ser Ala Leu Asp Pro Leu Ala Asp Lys Ile Leu
 160 165 170 175

Leu Ser Leu Leu Trp Val Ser Leu Thr Tyr Ala Arg Leu Ile Trp Val
 180 185 190 195

211 212 213
 Lys Tyr Phe Asn Pro Cys Tyr Ala Thr Ala Arg Leu Lys Pro Thr Phe
 225 230 235 240
 Ile Ser Lys Val Asn Thr Ala Val Gln Leu Ile Leu Val Ala Ala Ser
 245 250 255
 Leu Ala Ala Pro Val Phe Asn Tyr Ala Asp Ser Ile Tyr Leu Gln Ile
 260 265 270
 Leu Trp Cys Phe Thr Ala Ile Thr Thr Ala Ala Ser Ala Tyr Ser Tyr
 275 280 285
 Tyr His Tyr Gly Arg Lys Thr Val Gln Val Ile Lys Asp
 290 295 300

<210> 1
 <211> 353
 <212> 1KT
 <213> Homo sapiens

<400> 5
 Met Glu Ala Leu Gly Lys Leu Lys Gln Phe Asp Ala Tyr Pro Lys Thr
 1 5 10 15
 Leu Glu Asp Phe Arg Val Lys Thr Cys Gly Gly Ala Thr Val Thr Ile
 20 25 30
 Val Ser Gly Leu Leu Met Leu Leu Leu Phe Leu Ser Glu Leu Gln Tyr
 35 40 45
 Tyr Leu Thr Thr Glu Val His Pro Glu Leu Tyr Val Asp Lys Ser Arg
 50 55 60
 Gly Asp Lys Leu Lys Ile Asn Ile Asp Val Leu Phe Pro His Met Pro
 65 70 75 80
 Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp Val Ala Gly Glu Gln Gln
 85 90 95
 Leu Asp Val Ala His Asn Leu Ile Lys Ala Asn Leu Asp Lys Asp Lys
 100 105 110 115
 Leu Ile Val Ser Ser Glu Ala Ala Asn His Leu Leu Gly Lys Val Thr
 120 125 130 135
 Val Thr Val Ile Asp Ile Asp Ser Leu Asp Pro Asp Arg Tyr Gln Ser
 140 145 150
 Tyr Tyr Gly Ala Ala Ala Ala Asp Ile Lys Lys Tyr Asn Thr Tyr Ile

Asp Thr Ile Glu Gln Cys Arg Arg Gln Gly Phe Ser Val Lys Met Gln
180 185 190

Val Asn Lys Asn Glu Gly Cys Val Val Tyr Gly Phe Leu Ala Val Asn
195 200 205

Lys Val Ala Gly Asn Phe His Phe Ala Trp Gly Lys Ser Phe Val Gln
210 215 220

Ser His Val His Val His Asp Leu Gln Ser Phe Gly Leu Asp Asn Ile
225 230 235 240

Asn Met Thr His Tyr Ile Gln His Leu Ser Phe Gly Glu Asp Tyr Pro
245 250 255

Gly Ile Val Asn Pro Leu Asp His Thr Asn Val Thr Ala Pro Val Ala
260 265 270

Ser Met Met Phe Gln Tyr Phe Val Lys Val Val Pro Thr Val Tyr Met
275 280 285

Lys Val Asp Gly Glu Val Leu Arg Thr Asn Gln Phe Ser Val Thr Arg
290 295 300

His Glu Lys Val Ala Asn Gly Leu Leu Gly Asp Gln Gly Leu Pro Gly
305 310 315 320

Val Phe Val Leu Tyr Glu Leu Ser Pro Met Met Val Lys Leu Thr Glu
325 330 335

Lys His Arg Ser Phe Thr His Phe Leu Thr Gly Val Cys Ala Ile Ile
340 345 350

Gly Gly Met Phe Thr Val Ala Gly Leu Ile Asp Ser Leu Ile Tyr His
355 360 365

Ser Ala Arg Ala Ile Gln Lys Lys Ile Asp Leu Gly Lys Thr Thr
370 375 380

385-400

385-400

385-400

385-400

385-400

Met Thr Arg Leu Leu Gly Tyr Val Asp Trp Leu Asp Trp Ser Phe Val
405 410 415 420

Ala Ala Val Ile Thr Ile Thr Trp Asn Trp Leu Tyr Thr Asn Val Val
425 430 435 440

Ile Leu Arg Ser His Cys Phe Thr Glu Ala Met Leu Ser Ala Pro Arg
65 70 75 80

Met Glu Ser Leu Asp Thr Pro Ala Ala Tyr Ser Leu Gly Leu Ala Leu
85 90 95 100

Leu Gly Leu Gly Val Val Leu Val Leu Ser Ser Phe Phe Ala Leu Gly
105 110 115 120

Phe Ala Gly Thr Phe Leu Gly Asp Tyr Phe Gly Ile Leu Lys Glu Ala
125 130 135 140

Arg Val Thr Val Phe Pro Phe Asn Ile Leu Asp Asn Pro Met Tyr Trp
145 150 155 160

Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile Met His Ala Ser Pro
165 170 175 180

Thr Gly Leu Leu Leu Thr Val Leu Val Ala Leu Thr Tyr Ile Val Ala
185 190 195

Leu Leu Tyr Glu Glu Pro Phe Thr Ala Glu Ile Tyr Arg Glu Lys Ala
200 205 210 215

Ser Gly Ser His Lys Arg Ser
220 225

<210> ?

<211> 229

<212> HRT

<213> Homo sapiens

<400> ?

Met Ala Pro His Gly Pro Gly Ser Leu Thr Thr Leu Val Pro Trp Ala
1 5 10 15

Ala Ala Leu Leu Leu Ala Leu Gly Val Glu Arg Ala Leu Ala Leu Pro
20 25 30

Val Ile Cys Ile Thr Tyr Ser Gly Ser Thr Ala Asn Ile Ser Lys Val
35 40 45

Ala Ile Tyr Tyr Lys Thr Leu Asn Ile Ile Met Ile His Ala Asn Tyr
50 55 60

Tyr Leu Asn Ala Lys Gly Thr Ile Leu Gly Leu Asp Leu Glu Asn Tyr
65 70 75 80

Arg Ile Glu Asp Ile Gly Ile Asn Ile His Ala Ala His Ile Thr Val
85 90 95

116 120 124
 Asn Cys Ile Gly Gly Ile Asn Ala Trp Asn Thr Ile Thr Ser Tyr Ile
 137 138 140
 Asp Asn Gln Ile Cys Gln Gly Gln Lys Asn Leu Tyr Asn Asn Thr Gly
 145 150 155 16
 Asp Ile Gln Met Cys Pro Gln Asn Gly Ser Cys Val Pro Asp Gly Pro
 165 170 175
 Gly Leu Leu Gln Cys Val Cys Ala Asp Gly His His Gly Tyr Lys Cys
 180 185 190
 Met Arg Gln Gly Ser Phe Ser Leu Leu Met Phe Phe Gly Ile Leu Gly
 195 200 205
 Ala Thr Thr Leu Ser Val Ser Ile Leu Leu Trp Ala Thr Gln Arg Arg
 210 215 220
 Lys Ala Lys Thr Ser
 225

 <210> *
 <211> 178
 <212> PRT
 <213> Homo sapiens

 <400> *
 Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile
 1 5 10 15
 Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser
 20 25 30
 Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp
 35 40 45
 Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro
 50 55
 Ala Asp Ala Thr Ile Gln Ile Gln Thr Gln Thr Ala Thr Leu Ala Gly
 60
 Leu Asp Gly Ile Leu Val Thr Asp Ile Gln Thr His Lys Val Thr Lys
 65 70
 Ala Ala His Pro Thr Asp Asp Thr Thr Thr Leu Ser His Arg Pro Ser
 75 80 85
 Pro Ser Thr Asp Val Gln Thr Asp Ile Gln Thr Leu Lys Ile Leu Gly
 90

Arg Gly Leu Leu Val Ala Ala Val Leu Ile Ile Thr Gly Ile Ile Ile
141 142 143 144 145

Leu Thr Ser Gly Lys Cys Arg Gln Leu Ser Arg Leu Cys Arg Asn His
146 147 148 149 150

Cys Arg

151-152

153-154

155-156

157-158

159-160

Met Arg Leu Thr Arg Lys Arg Leu Cys Ser Ile Leu Ile Ala Leu Tyr
161 162 163 164 165 166 167 168 169 170

Cys Leu Ile Ser Leu Tyr Ala Ala Tyr His Val Ile Ile Gly Arg Arg
171 172 173 174 175 176 177 178 179 180

Arg Gln Ala Pro Ala Gly Ser Pro Arg Gly Leu Arg Lys Gly Ala Ala
181 182 183 184 185 186 187 188 189 190

Pro Ala Arg Gln Arg Arg Gly Arg Gln Gln Ser Thr Leu Glu Ser Glu
191 192 193 194 195 196 197 198 199 200

Glu Trp Asn Pro Trp Glu Gly Asp Glu Lys Asn Glu Gln Gln His Arg
201 202 203 204 205 206 207 208 209 210

Ile Lys Thr Ser Leu Gln Ile Leu Asp Lys Ser Thr Lys Gly Lys Thr
211 212 213 214 215 216 217 218 219 220

Asp Leu Ser Val Gln Ile Trp Gly Lys Ala Ala Ile Gly Leu Tyr Leu
221 222 223 224 225 226 227 228 229 230

Trp Gln His Ile Ile Gln Gly Leu Leu Asp Pro Ser Asp Val Thr Ala
231 232 233 234 235 236 237 238 239 240

Gln Thr Arg Gln Gly Lys Ser Ile Val Gly Asn Thr Gln Tyr Ser Ile
241 242 243 244 245 246 247 248 249 250

Leu Thr Asp Ile Ala Val Ile Ile Lys Tyr Ile Ser Val Arg Val Arg
251 252 253 254 255 256 257 258 259 260

Asn Val Val Leu Ile Leu Asn Lys Arg Ile Lys Ala Lys Ile Ile Tyr
261 262 263 264 265 266 267 268 269 270

Ala Thr Gln Thr Leu Leu Tyr Ala Gln Asn Leu Val Gln Ile Gln Lys
271 272 273 274 275 276 277 278 279 280

281-282 283-284 285-286 287-288 289-290 291-292 293-294 295-296

Leu Ile Ile Ile Tyr Asp Ser Ile Trp Ile Asn Asp Val Asp Val Ile
325 230 240 240

Gln Trp Pro Leu Gly Val Ala Thr Tyr Arg Asn Ile Pro Val Val Gln
340 350 355

Ala Ser Trp Ser Met Leu His Asp Gln Arg Ile Tyr Leu Cys Asn Ile
260 265 270

Leu Gly Thr Ile Tyr Gln Asn Ser Ser Arg Gln Ala Leu Met Asn Ile
275 280 285

Leu Lys Lys Asp Gly Asn Asp Lys Leu Cys Trp Val Ser Ala Arg Gln
290 295 300

His Trp Gln Pro Gln Gln Thr Asn Gln Ser Leu Lys Asn Tyr Gln Asp
305 310 315 320

Ala Leu Leu Gln Ser Asp Leu Thr Leu Cys Pro Val Gly Val Asn Thr
325 330 335

Glu Cys Tyr Arg Ile Tyr Glu Ala Cys Ser Tyr Gly Ser Ile Pro Val
340 345 350

Val Glu Asp Val Met Thr Ala Gly Asn Cys Gly Asn Thr Ser Val His
355 360 365

His Gly Ala Pro Leu Gln Leu Leu Lys Ser Met Gly Ala Pro Phe Ile
370 375 380

Phe Ile Lys Asn Trp Lys Glu Leu Pro Ala Val Leu Gln Lys Gln Lys
385 390 395 400

Thr Ile Ile Leu Gln Glu Lys Ile Glu Arg Arg Lys Met Leu Leu Gln
405 410 415

Trp Tyr Gln His Phe Lys Thr Glu Leu Lys Met Lys Phe Thr Asn Ile
420 425 430

Leu Ala Ser Ser Ile Leu Met Asn Asn Lys Ser
435 440

445-450

451-455

456-460

461-465: Homo sapiens

466-470

Met Ala Thr Ile Gly Ala Leu Leu Val Ile Ile Ile Ile Ile Ile Ser
475 480 485 490 495

40 41 42
 Leu Leu Ala Asn Arg Leu Thr Cys Ser Lys Ala Arg Ala Ala Asp Ala
 10 20 30 40 50
 Val Val Thr Thr Ile Arg Met Glu Ser Asn Leu Tyr Ala Asp Ala Ser
 60 70 80 90 100
 His Asp Lys Arg Glu Lys Lys Glu Ala Lys Glu Lys Glu Glu Lys Arg
 110 120 130 140 150
 Lys Lys Glu Lys Lys Thr Ala Lys Glu Gly Glu Ser Asn Leu Gly Leu
 160 170 180 190 200
 Asp Leu Glu Glu Lys Glu Pro Gly Asp His Glu Arg Ala Lys Ser Thr
 210 220 230 240 250
 Val Met
 260

<210> 11
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 11
 atgaaggatg tgaagatgga cctgttgatg gcagggttgg cctgagagc aggaactgac 60
 ctgtgtgtgt aactatgaa agaacaggtg agcaacgagg actgactgaa ggtgaagac 120
 tgaatgagc tggggagaa gtgtggacc gggcgcaccc gagggttgg cctacttacc 180
 gtaataacc aagttatag ctggaactgc gtggatgact cacaagacta ctactgttt 240
 aagaagaaa taagtgtt tttacagac ttgtgcaacg ccagcggggc caatgacct 300
 agtgggtg agtctatc tgggtgac actgactgac gttgtgtt ttgggttacc 360
 ggcagata

<1> 11
 <11> 369
 <112> DNA
 <113> Homo sapiens

<400> 11
 atgaaggatg tgaagatgga cctgttgatg gcagggttgg cctgagagc aggaactgac 60
 ctgtgtgtgt aactatgaa agaacaggtg agcaacgagg actgactgaa ggtgaagac 120

<1> 11 <11> 369 <112> DNA <113> Homo sapiens

gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 300
 gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 400
 gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 500
 gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 600
 gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 700
 gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 800

<210> 13
 <211> 243
 <212> DNA
 <213> Homo sapiens

<400> 13
 atgggagatc aggggggagg tggggggggg attggtgatga aggggggggg gggggggggg 60
 gggggggggg tggggggggg gggggggggg gggggggggg gggggggggg 120
 tggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 180
 gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 240
 gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 300

<210> 14
 <211> 903
 <212> DNA
 <213> Homo sapiens

<400> 14
 atgggagatc aggggggagg tggggggggg attggtgatga aggggggggg gggggggggg 60
 gggggggggg tggggggggg gggggggggg gggggggggg gggggggggg 120
 gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 180
 gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 240
 gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 300
 gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 360
 gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 420
 gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 480

[illegible]

4 3 4 4

Species	16
Year	1997
Sex	MALE
Genus	Homo sapiens

1470 16
 atgacacggg tggtagggata aatgacacac atgacacac gtttaggac tggtaggata 17
 aatgacacac tggtagggat atgacacac atgtaggac atgacacac tggtaggata 18
 aagtttagga gggcaattggt atgacacac atgtaggac atgtaggac tggtaggata 19
 atgacacgga aattaatgga atgacacac atgtaggac atgtaggac tggtaggata 20
 atggagagac tggacacacac agggggatg atgtaggac atgtaggac tggtaggata 21
 gtaggtatag tggatatacag attattttaa atgtaggac atgtaggac tggtaggata 22
 taatttagga tgcataagga gggagagatg atgtaggac atgtaggac tggtaggata 23
 cccatgtact ggggaagcac agcacaattac atgtaggac atgtaggac tggtaggata 24
 aagggcctgc tgcctgacggt gctgggtggc atgtaggac atgtaggac tggtaggata 25
 gaccccttca cccctgagat ctaccgggag aaatctatag ctgacacac gtaggata 26

```
<210> 17
<211> 687
<212> DNA
<213> Homo sapiens
```

[illegible]

atggaggggt ttaattttaa gatttt

ctt

*210 + 14
 *211 + 344
 *212 + LNA
 *213 + Homo sapiens

*430 + 14
 atggaggggt atggaggggt gttttttttt aattttttt gttttttt tttttttt 60
 tttttttt tttttttt tttttttt tttttttt tttttttt tttttttt 120
 tttttttt tttttttt tttttttt tttttttt tttttttt tttttttt 180
 tttttttt tttttttt tttttttt tttttttt tttttttt tttttttt 240
 atggaggggt tttttttt tttttttt tttttttt tttttttt tttttttt 300
 tttttttt tttttttt tttttttt tttttttt tttttttt tttttttt 360
 tttttttt tttttttt tttttttt tttttttt tttttttt tttttttt 420
 atggaggggt tttttttt tttttttt tttttttt tttttttt tttttttt 480
 tttttttt tttttttt tttttttt tttttttt tttttttt tttttttt 534

*210 + 14
 *211 + 1520
 *212 + LNA
 *213 + Homo sapiens

*430 + 14
 atggaggggt atggaggggt gttttttttt aattttttt gttttttt tttttttt 60
 tttttttt tttttttt tttttttt tttttttt tttttttt tttttttt 120
 tttttttt tttttttt tttttttt tttttttt tttttttt tttttttt 180
 tttttttt tttttttt tttttttt tttttttt tttttttt tttttttt 240
 tttttttt tttttttt tttttttt tttttttt tttttttt tttttttt 300
 tttttttt tttttttt tttttttt tttttttt tttttttt tttttttt 360
 atggaggggt tttttttt tttttttt tttttttt tttttttt tttttttt 420
 tttttttt tttttttt tttttttt tttttttt tttttttt tttttttt 480
 tttttttt tttttttt tttttttt tttttttt tttttttt tttttttt 534

[illegible]

<210> 20
<211> 390
<212> DNA.
<213> Homo sapiens

```

1437: 20
atggagacac tgggggacac tacggatgatg gagttt caga taccttcccc gttgaggag 60
caggaggccc aggaatctcg tacgaaacag tgggtt gttg taccttctctg gttataggc 120
ttccggttaa tgggttatctt ggtcttggatg ggcacaggcc ttctgt gttt caggggcag 180
gttggggag agggggag caggtt caga aggggttccc acctatcccc agacatggt 240
gaaacacag cagatcagaa agaggacaa cagacagaa agaaaggga caggaggaa 300
atctctca cctctctc tctctctc cctctctc cctctctc cctctctc
tctctctc tctctctc tctctctc tctctctc tctctctc tctctctc

```

1. 1990年12月
 2. 1991年12月
 3. 1992年12月
 4. 1993年12月

100

[illegible]

119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140
 Leu Ala Leu Ala Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala
 15 20 25

Arg His Leu Ser Thr Val Gln Ile Asp Met Ala Asn Lys
Gln Val Ser Asn Glu Asp Cys Leu Gln Val Phe Lys Asn Cys Thr Gln Leu

(6) (35) (40)

Gly Gly Glu Tyr Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr
45 50 55 60

Proteinase B cleavage site: Val⁶⁰-Ile⁶¹-Ser⁶²-Lys⁶³-Gly⁶⁴-Cys⁶⁵-Ser⁶⁶-Ileu⁶⁷-Asn⁶⁸-Cys⁶⁹-Val⁷⁰-Asp⁷¹-Asp⁷²-Ser⁷³-Gln⁷⁴-Asp⁷⁵

Tyr Tyr Val Gly Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys

80 85 90

Asn Ala Ser Gly Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala 339
95 100 105

Stg ctc cct gca ctc ggc cgg cgg cgc tgg gga cgc ggc gag cta 164
 Leu Leu Pro Ala Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu
 110 115 120

estrela da qual se trata, e a distância da estrela ao planeta, 524

adgtst jant at y rgt st gdrctdgt rrt drcm pccctmca tyy wctt 664

[illegible]

placemat the thoughtless, headstrong, ambitious, ambitious of history, and

Journal of Management Education 36(7) 809-824

[illegible]

84 Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
 1 1 1 13
 Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn
 24 34 44
 Glu Asp Cys Leu Gln Val Lys Asn Cys Thr Gln Leu Gly Gln Gln Cys
 5 41 41
 Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
 51 61 61
 Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly
 66 71 71 81
 Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly
 81 91 91
 Ala His Ala Ile Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala
 100 105 110
 Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu
 115 120

<210> 23
 <211> 1179
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (221)..(837)

<40> 2
 agggccagag cagggggg cagggggg cagggggg cagggggg cagggggg 60

cggggggg gggggggg gggggggg gggggggg gggggggg gggggggg 120

gggggggg gggggggg gggggggg gggggggg gggggggg gggggggg 180

gggggggg gggggggg gggggggg gggggggg gggggggg gggggggg 240
 gggggggg gggggggg gggggggg gggggggg gggggggg gggggggg 300
 gggggggg gggggggg gggggggg gggggggg gggggggg gggggggg 360

gggggggg gggggggg gggggggg gggggggg gggggggg gggggggg 420
 Gly Leu Gln Ile Thr Gly Thr Ala Leu Ala Val Leu Gly Thr Leu Gly
 43 53 63 73 83 93

gggggggg gggggggg gggggggg gggggggg gggggggg gggggggg 480
 Thr Ile Val Cys Cys Ala Leu Ile Ser Thr Arg Val Ser Ala Ile Ile

437
 Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Pys Lys Val Tyr Asp
 55 60 65

476
 Ser Leu Leu Ala Leu Ile Gln Asp Leu Gln Ala Ala Arg Ala Leu Ile
 70 75 80

504
 Val Val Ala Ile Leu Leu Ala Ala Phe Gly Leu Leu Val Ala Leu Val
 85 90 95

543
 Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala Lys Ala Lys
 100 105 110 115

600
 Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala Leu Leu Thr
 120 125 130

668
 Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg Asp Phe Tyr
 135 140 145

716
 Asn Pro Val Val Pro Gln Ala Gln Lys Arg Gln Met Gly Ala Gly Leu
 150 155 160

764
 Tyr Val Gly Trp Ala Ala Ala Ala Leu Gln Leu Leu Gly Gly Ala Leu
 165 170 175

812
 Leu Cys Cys Ser Cys Pro Pro Arg Glu Lys Lys Tyr Thr Ala Thr Lys
 180 185 190 195

860
 Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Pro Gly Ala Ser Leu Gly
 200 205 210

908
 Val Gly Tyr Arg Ala Arg Arg Arg Tyr Thr
 215 220 225 230

956
 Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Pro Gly Ala Ser Leu Gly
 235 240 245 250

1004
 Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Pro Gly Ala Ser Leu Gly
 255 260 265 270

1052
 Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Pro Gly Ala Ser Leu Gly
 275 280 285 290

1100
 Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Pro Gly Ala Ser Leu Gly
 295 300 305 310

1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100. 101. 102. 103. 104. 105. 106. 107. 108. 109. 110. 111. 112. 113. 114. 115. 116. 117. 118. 119. 120. 121. 122. 123. 124. 125. 126. 127. 128. 129. 130. 131. 132. 133. 134. 135. 136. 137. 138. 139. 140. 141. 142. 143. 144. 145. 146. 147. 148. 149. 150. 151. 152. 153. 154. 155. 156. 157. 158. 159. 160. 161. 162. 163. 164. 165. 166. 167. 168. 169. 170. 171. 172. 173. 174. 175. 176. 177. 178. 179. 180. 181. 182. 183. 184. 185. 186. 187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400. 401. 402. 403. 404. 405. 406. 407. 408. 409. 410. 411. 412. 413. 414. 415. 416. 417. 418. 419. 420. 421. 422. 423. 424. 425. 426. 427. 428. 429. 430. 431. 432. 433. 434. 435. 436. 437. 438. 439. 440. 441. 442. 443. 444. 445. 446. 447. 448. 449. 450. 451. 452. 453. 454. 455. 456. 457. 458. 459. 460. 461. 462. 463. 464. 465. 466. 467. 468. 469. 470. 471. 472. 473. 474. 475. 476. 477. 478. 479. 480. 481. 482. 483. 484. 485. 486. 487. 488. 489. 490. 491. 492. 493. 494. 495. 496. 497. 498. 499. 500. 501. 502. 503. 504. 505. 506. 507. 508. 509. 510. 511. 512. 513. 514. 515. 516. 517. 518. 519. 520. 521. 522. 523. 524. 525. 526. 527. 528. 529. 530. 531. 532. 533. 534. 535. 536. 537. 538. 539. 540. 541. 542. 543. 544. 545. 546. 547. 548. 549. 550. 551. 552. 553. 554. 555. 556. 557. 558. 559. 560. 561. 562. 563. 564. 565. 566. 567. 568. 569. 570. 571. 572. 573. 574. 575. 576. 577. 578. 579. 580. 581. 582. 583. 584. 585. 586. 587. 588. 589. 590. 591. 592. 593. 594. 595. 596. 597. 598. 599. 600. 601. 602. 603. 604. 605. 606. 607. 608. 609. 610. 611. 612. 613. 614. 615. 616. 617. 618. 619. 620. 621. 622. 623. 624. 625. 626. 627. 628. 629. 630. 631. 632. 633. 634. 635. 636. 637. 638. 639. 640. 641. 642. 643. 644. 645. 646. 647. 648. 649. 650. 651. 652. 653. 654. 655. 656. 657. 658. 659. 660. 661. 662. 663. 664. 665. 666. 667. 668. 669. 670. 671. 672. 673. 674. 675. 676. 677. 678. 679. 680. 681. 682. 683. 684. 685. 686. 687. 688. 689. 690. 691. 692. 693. 694. 695. 696. 697. 698. 699. 700. 701. 702. 703. 704. 705. 706. 707. 708. 709. 710. 711. 712. 713. 714. 715. 716. 717. 718. 719. 720. 721. 722. 723. 724. 725. 726. 727. 728. 729. 730. 731. 732. 733. 734. 735. 736. 737. 738. 739. 740. 741. 742. 743. 744. 745. 746. 747. 748. 749. 750. 751. 752. 753. 754. 755. 756. 757. 758. 759. 760. 761. 762. 763. 764. 765. 766. 767. 768. 769. 770. 771. 772. 773. 774. 775. 776. 777. 778. 779. 780. 781. 782. 783. 784. 785. 786. 787. 788. 789. 790. 791. 792. 793. 794. 795. 796. 797. 798. 799. 800. 801. 802. 803. 804. 805. 806. 807. 808. 809. 810. 811. 812. 813. 814. 815. 816. 817. 818. 819. 820. 821. 822. 823. 824. 825. 826. 827. 828. 829. 830. 831. 832. 833. 834. 835. 836. 837. 838. 839. 840.

100

- 2013 : 24
- 2012 : 210
- 2011 : 187
- 2010 : 1100 (H.100) *Small Islands*

1. 400 2. 200 3. 100 4. 50 5. 25 6. 12.5 7. 6.25 8. 3.125 9. 1.5625 10. 0.78125 11. 0.390625 12. 0.1953125 13. 0.09765625 14. 0.048828125 15. 0.0244140625 16. 0.01220703125 17. 0.006103515625 18. 0.0030517578125 19. 0.00152587890625 20. 0.000762939453125 21. 0.0003814697265625 22. 0.00019073486328125 23. 9.5367431640625E-05 24. 4.76837158203125E-05 25. 2.384185791015625E-05 26. 1.1920928955078125E-05 27. 5.9604644775390625E-06 28. 2.9802322387695312E-06 29. 1.4901161193847656E-06 30. 7.450580596923828E-07 31. 3.725290298461914E-07 32. 1.862645149230957E-07 33. 9.313225746154785E-08 34. 4.656612873077392E-08 35. 2.328306436538696E-08 36. 1.164153218269348E-08 37. 5.82076609134674E-09 38. 2.91038304567337E-09 39. 1.455191522836685E-09 40. 7.275957614183425E-10 41. 3.637978807091712E-10 42. 1.818989403545856E-10 43. 9.09494701772928E-11 44. 4.54747350886464E-11 45. 2.27373675443232E-11 46. 1.13686837721616E-11 47. 5.6843418860808E-12 48. 2.8421709430404E-12 49. 1.4210854715202E-12 50. 7.105427357601E-13 51. 3.5527136788005E-13 52. 1.77635683940025E-13 53. 8.88178419700125E-14 54. 4.440892098500625E-14 55. 2.2204460492503125E-14 56. 1.1102230246251562E-14 57. 5.551115123125781E-15 58. 2.7755575615628906E-15 59. 1.3877787807814453E-15 60. 6.938893903907226E-16 61. 3.469446951953613E-16 62. 1.7347234759768065E-16 63. 8.673617379884032E-17 64. 4.336808689942016E-17 65. 2.168404344971008E-17 66. 1.084202172485504E-17 67. 5.42101086242752E-18 68. 2.71050543121376E-18 69. 1.35525271560688E-18 70. 6.7762635780344E-19 71. 3.3881317890172E-19 72. 1.6940658945086E-19 73. 8.470329472543E-20 74. 4.2351647362715E-20 75. 2.11758236813575E-20 76. 1.058791184067875E-20 77. 5.293955920339375E-21 78. 2.6469779601696875E-21 79. 1.3234889800848437E-21 80. 6.617444900424219E-22 81. 3.3087224502121095E-22 82. 1.6543612251060547E-22 83. 8.271806125530273E-23 84. 4.1359030627651365E-23 85. 2.0679515313825682E-23 86. 1.0339757656912841E-23 87. 5.1698788284564205E-24 88. 2.5849394142282102E-24 89. 1.2924697071141051E-24 90. 6.4623485355705255E-25 91. 3.2311742677852627E-25 92. 1.6155871338926314E-25 93. 8.077935669463157E-26 94. 4.0389678347315785E-26 95. 2.0194839173657892E-26 96. 1.0097419586828946E-26 97. 5.048709793414473E-27 98. 2.5243548967072365E-27 99. 1.2621774483536182E-27 100. 6.310887241768091E-28 101. 3.1554436208840455E-28 102. 1.5777218104420227E-28 103. 7.888609052210113E-29 104. 3.9443045261050565E-29 105. 1.9721522630525282E-29 106. 9.860761315262641E-30 107. 4.9303806576313205E-30 108. 2.4651903288156602E-30 109. 1.2325951644078301E-30 110. 6.1629758220391505E-31 111. 3.0814879110195752E-31 112. 1.5407439555097876E-31 113. 7.703719777548938E-32 114. 3.851859888774469E-32 115. 1.9259299443872345E-32 116. 9.629649721936172E-33 117. 4.814824860968086E-33 118. 2.407412430484043E-33 119. 1.2037062152420215E-33 120. 6.0185310762101075E-34 121. 3.0092655381050537E-34 122. 1.5046327690525269E-34 123. 7.523163845262634E-35 124. 3.761581922631317E-35 125. 1.8807909613156585E-35 126. 9.403954806578292E-36 127. 4.701977403289146E-36 128. 2.350988701644573E-36 129. 1.1754943508222865E-36 130. 5.8774717541114325E-37 131. 2.9387358770557162E-37 132. 1.4693679385278581E-37 133. 7.3468396926392905E-38 134. 3.6734198463196452E-38 135. 1.8367099231598226E-38 136. 9.183549615799113E-39 137. 4.5917748078995565E-39 138. 2.2958874039497782E-39 139. 1.1479437019748891E-39 140. 5.7397185098744455E-40 141. 2.8698592549372227E-40 142. 1.4349296274686114E-40 143. 7.174648137343057E-41 144. 3.5873240686715285E-41 145. 1.7936620343357642E-41 146. 8.968310171678821E-42 147. 4.4841550858394105E-42 148. 2.2420775429197052E-42 149. 1.1210387714598526E-42 150. 5.605193857299263E-43 151. 2.8025969286496315E-43 152. 1.4012984643248157E-43 153. 7.006492321624079E-44 154. 3.5032461608120395E-44 155. 1.7516230804060197E-44 156. 8.758115402030098E-45 157. 4.379057701015049E-45 158. 2.1895288505075245E-45 159. 1.0947644252537622E-45 160. 5.473822126268811E-46 161. 2.7369110631344055E-46 162. 1.3684555315672027E-46 163. 6.8422776578360135E-47 164. 3.4211388289180067E-47 1

Mon Tue Wed Thy Fri Sat Sun Mon Tue Wed Thy Fri Sat Sun Mon Tue Wed Thy Fri Sat Sun Mon Tue Wed Thy Fri Sat Sun
1 5 9 13 17 21 25 29 31 1 5 9 13 17 21 25 29 31 1 5 9 13 17 21 25 29 31 1 5 9 13 17 21 25 29 31

Trp Leu Gly Thr Ile Val Cys α -Cys Ala Ser Lys Met Trp Arg Val Ser

Ala Phe Ile Gly Ser Asn Ile His Thr Ser Gln Asn Ile Trp Gln Gly

Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys Cys

Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg
61 70 80

Ala Lea The Val Val Ala The Lea Lea Ala Ala The Fly Lea Lea Val
85 90 95

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Leu | Val | Gly | Ala | Gln | Cys | Thr | Asn | Cys | Val | Gln | Asp | Asp | Thr | Ala |
| 100 | | | | | | | | 105 | | | | | 110 | | |

Lys Ala Lys Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala
115 120 125

| Len | Len | Thy | Len | Val | Pro | Val | Sex | Thy | Sex | Als | Asn | Thy | Trp | Trp | Arg |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 137 | | | | | | 135 | | | | | 119 | | | | |

Asp Thr Tyr Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly
145 150 155 160

Ala Gly Leu Tyr Val Gly Trp Ala Ala Ala Ala Leu Gln Leu Leu Gly

Ser Leu Tyr Thr Gly Tyr Arg Arg Leu Arg Tyr Val
 100 101 102 103 104 105 106 107 108 109 110 111

Trp Gly Ile Val Gly Pro Leu Val Pro Trp Ile Ile Pro Lys Gly Pro
13 28 37

Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys Cys
31 40 49

Tyr Leu Ile Trp Leu Ile Ala Ile Leu Ala His Leu Asn Pro Leu Phe
53 61 70

Gly Pro Gln Leu Lys Asn Gln Thr Ile Trp Tyr Leu Lys Tyr His Trp
81 90 99 108

Pro

<210> 27

<211> 1057

<212> RNA

<213> Homo sapiens

<220>

<221> CDS

<222> (125)..(1027)

<400> 27

agtatggagg caacggtagc ccagtggtctg agtgggtgac gggctctcat ggagaagcgg 60

ctcgcacagt tccacgctcg ctgagctctc gccgcacagc acacagagga gggcgagcag 120

ggc att cta gcc ttg cgc gtc gcc cgc gcc tag tgg ggc gcc ctg gcc 169
Met Leu Ala Leu Arg Val Ala Arg Gly Ser Trp Gly Ala Leu Arg
1 5 10 15

ggc gcc att tag ggt ccg gcc acc cgg ccg att aac cga cgc gcc tag 217
Gly Ala Ala Trp Ala Pro Gly Thr Arg Pro Ser Lys Arg Arg Ala Cys
20 25 30

tgt gat tgg tgg cgc cgt gtc gcc tgc tgc ttg ggc tgc ctg tgc gaa 265
Trp Ala Leu Leu Pro Pro Val Pro Cys Cys Leu Gly Cys Leu Ala Glu
35 40 45

ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 315
Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe
50 55 60 65 70 75 80 85 90 95

ttt gat att gcc cgt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 365
Phe Glu Arg Asn His Cys Ser Gly Ala Gly Lys Ala Ala His Arg Pro
100 105 110 115 120 125 130 135 140 145

ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 415
Ala Ala Gly Ala Gly Ala Ala Ala His Ala His Gly Gly His Trp Gly
150 155 160 165 170 175 180 185 190 195

[illegible]

6111-12
 6111-13
 6111-14
 6111-15

6111-16

Met Leu Ala Leu Arg Val Ala Arg Gly Ser Thr Gly Ala Leu Arg Gly
 1 10 19

Ala Ala Thr Ala Ser Gly Ser Arg Ser Lys Arg Arg Ala Cys Thr
 20 29

Ala Leu Leu Ser Pro Val Ser Cys Cys Leu Gly Cys Leu Ala Glu Arg
 30 39 48

Thr Arg Leu Arg Pro Ala Ala Leu Gly Leu Arg Leu Ser Gly Ile Gly
 50 59 68

Glu Arg Asp His Cys Ser Gly Ala Gly Lys Ala Ala Pro Arg Pro Ala
 70 79 88 97

Ala Gly Ala Gly Ala Ala Ala Glu Ala Pro Gly Gly Glu Thr Gly Pro
 100 109 118

Ala Ser Thr Pro Ser Leu Tyr Glu Asn Pro Thr Thr Ile Pro Asn Met
 120 129 138

Leu Ser Met Thr Arg Ile Gly Leu Ala Pro Val Leu Gly Tyr Leu Ile
 140 149 158

Ile Glu Glu Asp Pro Asn Ile Ala Leu Gly Val Phe Ala Leu Ala Gly
 160 169 178

Leu Thr Asp Leu Leu Asp Gly Phe Ile Ala Arg Asp Thr Ala Asn Glu
 180 189 198

Arg Ser Ala Leu Gly Ser Ala Leu Asp Pro Leu Ala Asp Lys Ile Leu
 200 209 218

Ile Ser Ile Ser Thr Val Ser Leu Thr Tyr Ala Asp Leu Ile Pro Val
 220 229 238

Ile Ser Thr Thr Thr Ile Ile Ser Arg Arg Ala Thr Met Leu Ile Ala Ala
 240 249 258

Val His Tyr Val Arg Tyr Arg Thr Leu His Ser His Arg Thr Leu Ala
 260 269 278

Lys Tyr Ile Asn Pro Tyr Tyr Ala Thr Ala Arg Leu Lys His Thr Ile
 280 289 298

Leu Thr Cys Ile Thr Ala Thr Thr Ala Ala Ser Ala Tyr Ser Tyr
100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120

Tyr His Tyr Gly Arg Lys Thr Val Ala Val Ile Lys Asp
121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140

210 24
211 100
212 100A
213 Homo sapiens

220
221 CTS
222 (102)...(1170)

40 24
ctttttttttt ggggggggggg c atg gag agc atg gag agc atg gag gag ttc 11
Ser Ala Ala Leu Gly Lys Leu Lys Gln Phe
1 5 10

aat ggc ttc att gag aac ttt gag aac ttt cgg atc gag aac ttc ggc 99
Asp Ala Tyr Pro Lys Thr Leu Glu Asp Phe Arg Val Lys Thr Cys Gly
15 20 25

ggc ggc aac ggc aac att ggc aac ggc att ctc atg atg atg atg ttc 147
Gly Ala Thr Val Thr Ile Val Ser Gly Leu Leu Met Leu Leu Leu Phe
30 35 40

atg ttc gag atg gag tat tat ctc aac aac gag atg cat cat gag atc 195
Leu Ser Gln Leu Gln Tyr Tyr Leu Thr Thr Gln Val His Pro Gln Leu
45 50 55

aac atg aac agc ttc ggc ggc aac aac ctc gag atc aac atc ttc ata 243
Tyr Val Asp Lys Ser Arg Gly Asp Lys Leu Lys Ile Asn Ile Asp Val
6 11 16

ctt tat cgc aac atg cat ttt ggc tat ttc agt att gat gag atg gat 291
Leu Phe Pro His Met Pro Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp
21 26 31 36

ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 339
Val Ala Arg Val Val Val Val Val Val Val Val Val Val Val Val Val
34 39 44 49 54 59 64 69 74 79 84 89 94

ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 387
Arg Leu Arg Lys Asp Gly Ile Pro Val Ser Ser Gln Ala Gln Arg His
90 95 100 105 110 115 120 125 130 135 140 145 150 155

ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 435
Val Leu Arg Leu Thr His Val Thr Thr Ile Arg Leu Arg Ser Leu Arg
156 161 166 171 176 181 186 191 196 201 206 211 216 221

43 51 53 55 57 59 61 63 65 67 69 71 73 75 77 79 81 83 85 87 89 91 93 95 97 99 101 103 105 107 109 111 113 115 117 119 121 123 125 127 129 131 133 135 137 139 141 143 145 147 149 151 153 155 157 159 161 163 165 167 169 171 173 175 177 179 181 183 185 187 189 191 193 195 197 199 201 203 205 207 209 211 213 215 217 219 221 223 225 227 229 231 233 235 237 239 241 243 245 247 249 251 253 255 257 259 261 263 265 267 269 271 273 275 277 279 281 283 285 287 289 291 293 295 297 299 301 303 305 307 309 311 313 315 317 319 321 323 325 327 329 331 333 335 337 339 341 343 345 347 349 351 353 355 357 359 361 363 365 367 369 371 373 375 377 379 381 383 385 387 389 391 393 395 397 399 401 403 405 407 409 411 413 415 417 419 421 423 425 427 429 431 433 435 437 439 441 443 445 447 449 451 453 455 457 459 461 463 465 467 469 471 473 475 477 479 481 483 485 487 489 491 493 495 497 499 501 503 505 507 509 511 513 515 517 519 521 523 525 527 529 531 533 535 537 539 541 543 545 547 549 551 553 555 557 559 561 563 565 567 569 571 573 575 577 579 581 583 585 587 589 591 593 595 597 599 601 603 605 607 609 611 613 615 617 619 621 623 625 627 629 631 633 635 637 639 641 643 645 647 649 651 653 655 657 659 661 663 665 667 669 671 673 675 677 679 681 683 685 687 689 691 693 695 697 699 701 703 705 707 709 711 713 715 717 719 721 723 725 727 729 731 733 735 737 739 741 743 745 747 749 751 753 755 757 759 761 763 765 767 769 771 773 775 777 779 781 783 785 787 789 791 793 795 797 799 801 803 805 807 809 811 813 815 817 819 821 823 825 827 829 831 833 835 837 839 841 843 845 847 849 851 853 855 857 859 861 863 865 867 869 871 873 875 877 879 881 883 885 887 889 891 893 895 897 899 901 903 905 907 909 911 913 915 917 919 921 923 925 927 929 931 933 935 937 939 941 943 945 947 949 951 953 955 957 959 961 963 965 967 969 971 973 975 977 979 981 983 985 987 989 991 993 995 997 999

111-113
111-115
111-117
111-119

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Arg | Tyr | Val | His | Lys | Thr | Arg | Lys | Leu | Ser | Arg | Ala | His | Gly | Ser |
| | | | 45 | | | 40 | | | | | | 45 | | | |
| Asp | Tyr | Leu | Ala | Tyr | Tyr | Ser | Leu | Ser | Val | Thr | His | Leu | Leu | Leu | Asp |
| 55 | | | | | | 55 | | | | | | 60 | | | |
| Phe | Leu | Arg | Ser | His | Cys | Phe | Thr | His | Ala | Met | Leu | Ser | Gln | Pi | Arg |
| 65 | | | 70 | | | | | | 75 | | | 80 | | | |
| Met | Val | Ser | Leu | Asp | Thr | Ile | Ala | Ala | Tyr | Ser | Leu | Gly | Leu | Ala | Leu |
| | | | 85 | | | | | | 90 | | | 95 | | | |
| Leu | Gly | Leu | Gly | Val | Val | Leu | Val | Leu | Ser | Ser | Phe | Phe | Ala | Leu | Gly |
| 100 | | | | | | 105 | | | | | | 110 | | | |
| Phe | Ala | Gly | Thr | Phe | Leu | Gly | Asp | Tyr | Phe | Gly | Ile | Leu | Lys | Glu | Ala |
| 115 | | | | | | 120 | | | | | | 125 | | | |
| Arg | Val | Thr | Val | Phe | Pro | Phe | Asn | Ile | Leu | Asp | Asn | Ile | Met | Tyr | Trp |
| 130 | | | | | | 135 | | | | | | 140 | | | |
| Gly | Ser | Thr | Ala | Asn | Tyr | Leu | Gly | Trp | Ala | Ile | Met | His | Ala | Ser | Pro |
| 145 | | | 150 | | | | | | 155 | | | 160 | | | |
| Thr | Gly | Leu | Leu | Leu | Thr | Val | Leu | Val | Ala | Leu | Thr | Tyr | Ile | Val | Ala |
| | | | 165 | | | | | | 170 | | | 175 | | | |
| Leu | Leu | Tyr | Gln | Gln | Pro | Phe | Thr | Ala | Gln | Ile | Tyr | Arg | Gln | Lys | Ala |
| 180 | | | | | | 185 | | | | | | 190 | | | |
| Ser | Gly | Ser | His | Lys | Arg | Ser | | | | | | | | | |
| 195 | | | | | | | | | | | | | | | |

```
<210> 33
<211> 904
<212> DNA
<213> Homo sapiens
```

Mon. Tues. Wed. Thurs. Fri. Sat. Sun. Mon. Tues. Wed. Thurs. Fri. Sat. Sun.

Table 1. The number of cases of *Salmonella* infection in the United Kingdom, 1990-1999, by serotype and age group. The number of cases is given in parentheses. The percentage of cases is given in brackets. The number of cases is given in parentheses. The percentage of cases is given in brackets.

| Year | 1966 | 1967 | 1968 | 1969 | 1970 | 1971 | 1972 | 1973 | 1974 | 1975 | 1976 | 1977 | 1978 | 1979 | 1980 | 1981 | 1982 | 1983 | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| 1966 | 1967 | 1968 | 1969 | 1970 | 1971 | 1972 | 1973 | 1974 | 1975 | 1976 | 1977 | 1978 | 1979 | 1980 | 1981 | 1982 | 1983 | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 | |

Arg Lys Lys Ala Arg Ser Val Thr Phe Tyr Trp Met Ile Val
Asp Cys Cys Leu Asp Glu Asn Gly Thr Thr Trp Gly Leu Asp Val

L6 L7

Aug 07% Sep 10% Oct 0% Nov 0% Dec 0% Jan 0% Feb 0% Mar 0% Apr 0% May 0% Jun 0% Jul 0% Aug 0% Sep 0% Oct 0% Nov 0% Dec 0%

Aug 07% Sep 10% Oct 0% Nov 0% Dec 0% Jan 0% Feb 0% Mar 0% Apr 0% May 0% Jun 0% Jul 0% Aug 0% Sep 0% Oct 0% Nov 0% Dec 0%

481 gtr ata ata gac atg car pua uua uua cta aua ggt gac uuq gta 336
 Thr Val Ile Ile Asp Leu Gln Ala Asn Pro Leu Lys Gly Asp Leu Ala
 95 100 105 110

Ala Ser His Arg Gly Ile Met Cys His Arg Asn Gly Asn Gly Asn Ser 386
 Asn Thr Phe Arg Gly Phe Thr Gln Leu Gln Thr Leu Ile Leu Pro Gln
 115 120 125

Val Gln Asn Gln Ser Gln Gln Ala Val Gln Gln Asn Asn Asn Asn Asn 434
 His Val Asn Cys Pro Gly Gly Ile Asn Ala Trp Asn Thr Ile Thr Ser
 139 140

[illegible]

481 ggg gac cca gaa atg ttt ttt tat aat gga tat tgt gta gtt gat 131
 Thr Gly Asp Pro Glu Met Cys Pro Glu Asn Gly Ser Cys Val Pro Asp
 160 170

ggt cca ggt ctt ttg cag tgt gta tgt ggt gat ggt ttc cat gga tac 578
Gly Pro Gly Leu Leu Gln Cys Val Cys Ala Asp Gly Phe His Gly Tyr
175 180 185 190

aaq tgt atg cgc cag ggg tgg ttg tca atg att atg ttc ttc ggg att 626
Lys Cys Met Arg Gln Gly Ser Phe Ser Leu Leu Met Phe Phe Gly Ile
 195 200 205

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

1. The first group of variables includes the variables that are used to explain the dependent variable in the first equation of the system. These variables are the variables that are used to explain the dependent variable in the first equation of the system.

- 1990: 100% of the population had access to electricity
- 1990: 100% of the population had access to clean water
- 1990: 100% of the population had access to health care

1. *Chlorophyll a* and *Chlorophyll b* were determined by the method of Arar and Collins (1971).

Met Ala 1: His Gly Pro Gly Ser Leu Thr Thr Leu Val Pro Tyr Ala
 1 5 10 15

Ala Ala Leu Leu Leu Ala Leu Gly Val Glu Arg Ala Leu Ala Leu Pro
30 35 40

Glu Thr Cys Thr Glu Cys Pro Gly Ser Val Glu Asp Leu Ser Lys Val
 31 40 45

Ala Thr Tyr Asp Lys Thr Thr Arg Glu Leu Met Leu His Ala Arg Cys

Cys₁ Dec Jan Feb Mar Apr May Jun Jul Aug Sep Oct Nov Dec Cys₂
 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2

Zee 100 Gly Asp Pro Gly Pro Asp Tyr His Glu Ala His Thr Thr Val
 40 40 40

Ile Ile Asp Leu Gln Ala Asn Pro Leu Lys Gly Asp Leu Ala Asn Thr
100 105 110

Phe Arg Gly Phe Thr Gln Leu Gln Thr Leu Ile Leu Pro Gln His Val
115 120 125

Asn Cys Pro Gly Gly Ile Asn Ala Trp Asn Thr Ile Thr Ser Tyr Ile
130 135 140

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Asn | Gln | His | Pro | Gly | Glu | Gly | Glu | Leu | Ala | Val | Gly | Asn | Asn | Trp | Gly |
| 120 | 121 | 122 | 123 | 124 | 125 | 126 | 127 | 128 | 129 | 130 | 131 | 132 | 133 | 134 | 135 | 136 |

| Age | Sex | Q1 | Med | Q3 | Min | Q1 | Med | Q3 | Max | Q1 | Med | Q3 | Max | Q1 | Med | Q3 | Max |
|---------|-----|-----|-----|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 18-24 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 25-34 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 35-44 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 45-54 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 55-64 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 65-74 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 75-84 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 85-94 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 95-104 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 105-114 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 115-124 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 125-134 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 135-144 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 145-154 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 155-164 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 165-174 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 175-184 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 185-194 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 195-204 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 205-214 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 215-224 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 225-234 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 235-244 | F | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 245-254 | F | 1.0 | 1.0 | 1.0</ | | | | | | | | | | | | | |

Arg Leu Leu Glu Cys Val Cys Ala $\frac{1}{2}$ Arg Gly His His Gly Tyr Lys Cys

$$\frac{\partial}{\partial t} \left(\frac{1}{\rho} \right) + \frac{\partial}{\partial x} \left(\frac{v}{\rho} \right) = - \frac{1}{\rho^2} \left(v \frac{\partial \rho}{\partial x} + w \frac{\partial \rho}{\partial y} + u \frac{\partial \rho}{\partial z} \right)$$

02201-
02201 CTS
02201 (139)...(1572)

0471-35

0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35
Met Ser Leu Ser Gly Arg

1 1

0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 104
Leu Cys Leu Leu Thr Ile Val Gly Leu Ile Leu Leu Thr Thr Arg Gly Ile
10 10 10

0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 130
Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser Ala Asp Ser Thr Ile Met
20 20 20

0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 130
Asp Ile Gln Val Pro Thr Arg Ala Ile Asp Ala Val Tyr Thr Ile Leu
10 10 10

0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 240
Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro Ala Asp Gln Thr Pro Gln
30 30 30 30

0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 296
Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly Thr Asp Gly Pro Leu Val
70 70 70

0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 344
Thr Asp Pro Gln Thr His Lys Ser Thr Lys Ala Ala His Pro Thr Asp
90 90 100

0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 392
Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser Pro Ser Thr Asp Val Gln
105 110 115

0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 440
Thr Asp Pro Gln Thr Leu Lys Pro Ser Gly Phe His Glu Asp Asp Pro
120 125 130

0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 490
Ile Ile Tyr Arg His His Thr Leu Arg Arg Arg Arg Arg Arg Arg Arg
140 140 140 140 140 140 140 140 140 140

0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 540
Ala Val Leu Phe Ile Thr Gly Ile Ile Ile Leu Thr Thr Thr Gly Lys Tyr
150 150 150 150 150 150 150 150 150 150

0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 0471-35 590
Arg His Leu Ser Arg Leu Tyr Arg Arg His Tyr Arg
160 160 160 160 160 160 160 160 160 160

Phe Lys Thr Glu Leu Lys Met Lys Phe Thr Asn Ile Leu Val Ser Ser
411 42 436

111 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

<211> 3-
<211> 443
<212> 881
<213> Homo sapiens

<400> 1-
Met Arg Leu Thr Arg Lys Arg Leu Cys Ser Phe Leu Ile Ala Leu Tyr
1 1 1 11

Cys Leu Phe Ser Leu Tyr Ala Ala Tyr His Val Phe Phe Gly Arg Arg
20 25 3

Arg Gln Ala Pro Ala Gly Ser Pro Arg Gly Leu Arg Lys Gly Ala Ala
35 40 45

Pro Ala Arg Gln Arg Arg Gly Arg Gln Gln Ser Thr Leu Gln Ser Gln
50 55 60

Glu Trp Asn Pro Trp Glu Gly Asp Glu Lys Asn Glu Gln Gln His Arg
65 70 75 80

Phe Lys Thr Ser Leu Gln Ile Leu Asp Lys Ser Thr Lys Gly Lys Thr
85 90 95

Asp Leu Ser Val Gln Ile Trp Gly Lys Ala Ala Ile Gly Leu Tyr Leu
100 105 110

Trp Glu His Ile Phe Glu Gly Leu Leu Asp Pro Ser Asp Val Thr Ala
115 120 125

Gln Trp Arg Glu Gly Lys Ser Ile Val Gly Arg Thr Gln Tyr Ser Phe
130 135 140

145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995 1000

1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870 1871 1872 1873 1874 1875 1876 1877 1878 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438

238 239 240 241
 Ala Tyr Pro Leu Gly Val Ala Thr Tyr Arg Asn Ile Pro Val Val Gln
 241 242 243
 Ala Ser Thr Cys Met Leu His Asp Gln Arg Ile Tyr Leu Lys Asn Pro
 244 245 246
 Leu Gly Thr Ile Tyr Gln Asn Ser Ser Arg Gln Ala Leu Met Asn Ile
 247 248 249
 Leu Lys Lys Asp Gly Asn Asp Lys Leu Cys Trp Val Ser Ala Arg His
 250 251 252
 His Trp Gln Pro Ala Ala Thr Asn Gln Ser Leu Lys Asn Tyr Gln Asp
 253 254 255
 Ala Leu Leu Glu Ser Asp Leu Thr Leu Cys Pro Val Gly Val Asn Thr
 256 257 258
 Gln Cys Tyr Arg Ile Tyr Gln Ala Cys Ser Tyr Gly Ser Ile Pro Val
 259 260 261
 Val Gln Asp Val Met Thr Ala Gly Asn Cys Gly Asn Thr Ser Val His
 262 263 264
 His Gly Ala Pro Leu Gln Leu Leu Lys Ser Met Gly Ala Pro Phe Ile
 265 266 267
 Phe Ile Lys Asn Trp Lys Glu Leu Pro Ala Val Leu Glu Lys Glu Lys
 268 269 270
 Thr Ile Ile Leu Gln Glu Lys Ile Glu Arg Arg Lys Met Leu Leu Gln
 271 272 273
 Trp Tyr Gln His Ile Lys Thr Glu Leu Lys Met Lys Phe Thr Asn Ile
 274 275 276
 Leu Glu Ser Ser Phe Leu Met Asn Asn Lys Ser
 277 278

279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500

Pro Val Ala Ala Met Ala Ala Thr Ala His Arg Leu Lys Pro Thr Leu
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

Val Gly Leu Ala Ala Val Val Gly Phe Leu Phe Ile Val Tyr Leu Val
21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40

Leu Lys Ala Asn Arg Leu Thr Tyr Ser Lys Ala Arg Ala Val Asp His
41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60

Glu His Thr Thr Phe Arg Met Glu Ser Asn Leu Tyr Val Asp Glu Ser
61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80

Glu Asp Lys Arg Glu Lys Lys Glu Ala Lys Glu Lys Glu Glu Lys Arg
81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Lys Lys Glu Lys Lys Thr Ala Lys His Gly Ala Ser Asn Leu Gly Leu
101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120

Asp Leu His Glu Lys Glu Phe Gly Asp His Glu Arg Ala Lys Ser Thr
121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140

Val Met
141 142

<210> 41

<211> 14

<212> CNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chimeric
cDNA-RNA oligonucleotide

<400> 41

gggggagcttgaaggga

14

<210> 42

<211> 176

<212> ERT

<213> Artificial Sequence

<220>

Met Lys Ala Leu Leu Leu Ala Thr Thr Arg Ala Leu Leu Tyr Ala Ala
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

Arg Ala His Thr Leu Ile Tyr His Ser Tyr Ser Arg Ala Ser Ser Asn
21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40

Thr Ala Tyr Leu Thr Leu Val Lys Tyr Ala His Asn His His His Tyr
41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60

61
 Gly Ile Ala Ala Ala Ser Val Tyr Tyr Tyr Asp Ser Ile Leu Tyr Asn
 85 90 95

116 Ser Gly Ser Ser Ser Val Lys Ala Ser Tyr Ala Val Leu Ala Leu
 100 105 110

Gly Ile Leu Val Ser Phe Val Tyr Val Leu Arg Ala Arg His
 115 120 125

4210-41
 4211-417
 4212-187
 4213-Parus norvegicus

4400-41
 Met Ser Met Ser Leu Glu Ile Thr Gly Thr Ser Leu Ala Val Leu Gly
 1 5 10 15

Trp Leu Cys Thr Ile Val Cys Cys Ala Leu Pro Met Trp Arg Val Ser
 20 25 30

Ala Pro Ile Gly Ser Ser Ile Ile Thr Ala Gln Ile Thr Trp Gln Gly
 35 40 45

Leu Trp Met Asn Cys Val Gln Ser Thr Gly Gln Met Gln Cys Lys Met
 50 55 60

Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg Ala
 65 70 75 80

Leu Ile Val Val Ser Ile Leu Leu Ala Ala Phe Gly Leu Leu Val Ala
 85 90 95

Leu Val Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Gln Thr Ala Lys
 100 105 110

Ala Lys Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala Val
 115 120 125

Phe Thr Leu Val Ile Val Ser Thr Ser Ala Asn Thr Ile Leu Arg Arg
 130 135 140

Ile Tyr Ala Ile Ile Val Ile Ile Ala Ile Tyr Ala Ile Thr Ile Thr
 145 150 155

Gly Leu Tyr Val Gly Trp Ala Ala Ala Ala Leu Gln Leu Leu Gly Gly
 160 165 170

Ala Leu Ile Tyr Tyr Ser Asp Ile Ile Arg Ala Lys Tyr Ala Ser His

Gly Thr Ala Tyr Asp Arg Lys Thr Thr Ser Glu Arg Pro Gly Ala Arg
 110 115 120

Thr Pro His His His Tyr Gln His Met Ser Tyr His Thr
 125 130 135

210 44

211 90

212 FRK

213 Caenorhabditis elegans

400 44

Met Cys Asn His Ser Tyr Phe Gln Leu Val Met Gly Ile Leu Ile Pro
 1 10 15

Leu Val Ser Val Ser Ala Phe Trp Ala Ile Ile Gly His Gly Gly Pro
 20 25 30

Trp Ile Val Pro Lys Gly Pro Asn Arg Gly Ile Ile Gln Leu Met Ile
 35 40 45

Ile Met Thr Ala Val Cys Cys Trp Met Phe Trp Ile Met Val Phe Leu
 50 55 60

His Gln Leu Asn Pro Leu Ile Gly Pro Gln Ile Asn Val Lys Thr Ile
 65 70 75 80

Arg Trp Ile Ser Glu Lys Trp Gly Asp Ala Pro Asn Val Ile Asn Asn
 85 90 95

210 43

211 246

212 FRK

213 Caenorhabditis elegans

400 45

Met Ile Val Thr Ser Met Phe Arg Gly Ile Ala Cys Arg Cys Glu Leu
 1 5 10 15

Val Ile Thr Thr His Arg Arg Met Ser Arg Arg His Thr Thr Thr
 20 25 30 35 40

His Val Lys Val Ser His Lys Lys Val Ser Leu His His Val Ala Arg
 45 50 55 60 65

Gly Lys Tyr Lys Val Ala Thr Ile His Asn Ala Ile Tyr Thr Ala Arg
 70 75 80 85 90

Ile Ala Ala Thr His His Ile Lys Tyr Ser Val Val Thr His Asn Ile
 95 100 105

111 112 113
 Ser Val Leu Asp Pro Val Ala Asp Lys Leu Leu Ile Ser Thr Met Ile
 111 112 113
 114 Thr Met Thr Tyr Ala Gly Leu Ile Pro Leu Pr Leu Thr Ser Val
 114 115 116
 Val Ile Leu Arg Asp Ile Cys Leu Ile Gly Gly Gly Ile Tyr Lys Arg
 117 118 119
 Tyr Gln Val Met Ser Pro Pro Tyr Ser Leu Ser Arg Ile Phe Asn Pro
 120 121 122
 Gln Val Ser Ser Met Gln Val Val Pro Thr Met Met Ser Lys Ile Asn
 123 124 125
 Thr Val Leu Gln Ile Thr Leu Val Ala Leu Ser Leu Ser Ser Pro Val
 126 127 128
 Phe Asp Phe Ser Thr Gly Ala Asn Asp Val Ile Val Gly Leu Gly Cys
 129 130 131
 Ile Thr Gly Ile Thr Thr Ile Tyr Ser Gly Leu Gln Tyr Ala Ser Gly
 132 133 134
 Lys Ala Ile Lys Lys Ile
 135

<210> 46

<211> 440

<212> 1RT

<213> Caenorhabditis elegans

<400> 46

Met Ser Leu Leu Trp Ser Leu Lys His Phe Asp Ala Tyr Arg Lys Pro
 1 2 3 4 5 6 7 8 9 10 11
 Met Asp Asp Phe Arg Val Lys Thr Leu Ser Gly Gly Leu Val Thr Leu
 12 13 14 15 16 17 18 19 20 21 22
 Leu Ala Ile Leu Ala Ile Val Leu Ile Thr Leu Ile Thr Lys Ile
 23 24 25 26 27 28 29 30 31 32 33
 Leu Ile Ser Leu Val Thr Ile Val Glu Ile Thr Val Arg Val Thr Ile
 34 35 36 37 38 39 40 41 42 43 44
 Ser Asp Val Arg Val His Ile Val Ile Asp Ile Thr Ile Thr Lys Leu
 45 46 47 48 49 50 51 52 53 54 55
 Pr Tyr Arg Ile Ile Thr Val Arg Val Met Arg Val Ser Ser Val Ala

Gly Arg Asn Ile Ser Gln Ser Ala Gln Lys Ile Val Ile Asn Gln Asn
137 1 138

Lys Thr Ser Val Gln Thr Thr Asp Val Ile Gln His Val Lys Cys Gly
139 140 141

Ser Cys Tyr Gly Ala Ala Ala Asp Gly Ile Cys Cys Asn Thr Cys Asp
142 143 144 145 146

Asp Val Lys Ser Ala Tyr Ala Val Lys Gly Trp Gln Val Asn Ile Gln
147 148 149 150

Gln Val His Gln Cys Lys Asn Asp Lys Trp Val Lys Gln His Asn Gln
151 152 153

His Lys Asn Gln Gly Cys Arg Val Tyr Gly Thr Val Lys Val Ala Lys
154 155 156

Val Ala Gly Asn Phe His Leu Ala Phe Gly Asp Phe His Gln Ala Met
157 158 159

Arg Ser His Val His Asp Leu His Asn Leu Asp Pro Val Lys Phe Asp
160 161 162 163 164

Ala Ser His Thr Val Asn His Val Ser Phe Gly Lys Ser Phe Pro Gly
165 166 167 168

Lys Asn Tyr Pro Leu Asp Gly Lys Val Asn Thr Asp Asn Arg Gly Gly
169 170 171 172

Ile Met Tyr Gln Tyr Tyr Val Lys Val Val Pro Thr Arg Tyr Asp Tyr
173 174 175 176

Leu Asp Gly Arg Val Asp Gln Ser His Gln Phe Ser Val Thr Thr His
177 178 179 180

Lys Lys Asp Leu Gly Phe Arg Gln Ser Gly Leu Pro Gly Phe Phe Leu
181 182 183 184 185

Gln Tyr Gln Phe Ser Pro Leu Met Val Gln Tyr Gln Glu Phe Arg Gln
186 187 188 189

Ser His Ala Ser His Leu Val Ser Leu Tyr Ala Leu Val Lys Lys Val
190 191 192

His Ala Val Ala Ser His Thr Asp Ile Ser Ile Lys His Ala Ala Asp
193 194 195 196

Tyr Met Lys Ser Arg His Ala Gly Gly Lys Leu Thr
197 198 199

4.12.47

Ser Thr Leu Leu Gly Tyr Val Asp Pro Thr Glu Pro Ser Phe Val Ala
1 1 1 1

Ala Val Leu Thr Ile Val Phe Asn Pro Leu Phe Trp Asn Val Val Ala
22 25 30

Arg Trp Glu Glu Arg Thr Arg Lys Leu Ser Arg Ala Phe Gly Ser Pro
32 40 45

Tyr Leu Ala Cys Tyr Ser Leu Gly Ser Ile Ile Leu Leu Leu Asn Ile
51 57

Leu Arg Ser His Cys Phe Thr Glu Ala Met Met Ser Glu Pro Lys Met
65 70 73

Ala Gly Leu Asp Ser His Thr Ile Tyr Phe Leu Gly Leu Ala Leu Leu
85 90 93

Gly Trp Gly Leu Val Phe Val Leu Ser Ser Phe Tyr Ala Leu Gly Phe
100 105 110

Thr Gly Thr Phe Leu Gly Asp Tyr Phe Gly Ile Leu Lys Glu Ser Arg
115 120 125

Val Thr Thr Phe Pro Phe Ser Val Leu Asp Asn Pro Met Tyr Trp Gly
130 135 140

Ser Thr Ala Asn Tyr Leu Gly Trp Ala Leu Met His Ala Ser Pro Thr
145 150 155 160

Gly Leu Leu Leu Thr Val Leu Val Ala Leu Val Tyr Val Val Ala Leu
165 170 175

Leu Phe Glu Glu Pro Phe Thr Ala Glu Ile Tyr Arg Arg Lys Ala Thr
180 185 190

Arg Leu His Lys Arg Ser
195

4.12.48

4.12.49

4.12.50

4.12.51

4.12.52

Met Ser Leu Ser Ser Arg Leu Lys Leu Leu Thr Ile Val Ala Leu Ile
1 1 1 1

Leu Leu Ser Arg Gly Glu Tyr Leu Lys Lys Leu Ser Ser Ile Thr
1 1 1 1 1 1 1 1

81 82 83
 His Ala Thr Gly Ser His Thr Ala Ala Gln Thr Ala Thr Gln Gln Leu
 84 85 86
 Ser Lys Met Ala Thr Ser Asn Pro Val Ser Asp Pro Gly Pro His Thr
 87 88 89
 Ser Ser Lys Lys Gly Thr Pro Ala Val Ser Arg Ile Gln Pro Leu Ser
 90 91 92
 Pro Ser Lys Asn Phe Met Pro Pro Ser Tyr Ile Gln His Pro Leu Asp
 93 94 95
 Ser Asn Gln Asn Asn Pro Phe Tyr Tyr Asp Asp Thr Thr Leu Arg Lys
 96 97 98
 Arg Gly Leu Leu Val Ala Ala Val Leu Phe Ile Thr Gly Ile Ile Ile
 99 100 101
 Leu Thr Ser Gly Lys Cys Arg Gln Leu Ser Gln Phe Cys Leu Asn Arg
 102 103 104
 His Arg
 105 106 107

a'
 cat